

WEST Search History

DATE: Friday, January 14, 2005

Hide?	Set Name	Query	Hit Count
	<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=NO; OP=OR</i>		
<input type="checkbox"/>	L22	L21 and reflection	29
<input type="checkbox"/>	L21	l19 and (polymer near5 synthesis)	66
<input type="checkbox"/>	L20	(sensor adj matrix) and L19	1
<input type="checkbox"/>	L19	L18 and uv	289
<input type="checkbox"/>	L18	l15 and (ccd)	609
<input type="checkbox"/>	L17	6271957.pn.	2
<input type="checkbox"/>	L16	L15 near20(micro adj mirror adj array)	8
<input type="checkbox"/>	L15	(array\$ near20 photolithograph\$\$\$\$)	4734
<input type="checkbox"/>	L14	l11 and (reflection near matrix)	4
<input type="checkbox"/>	L13	L11 and l10	1
<input type="checkbox"/>	L12	L11 and l6	0
<input type="checkbox"/>	L11	(illumination near matrix)	115
<input type="checkbox"/>	L10	(light near sensor near matrix)	36
<input type="checkbox"/>	L9	L8 and l6	0
<input type="checkbox"/>	L8	ccd adj matrix	624
<input type="checkbox"/>	L7	ccd matrix	738652
<input type="checkbox"/>	L6	(micro near mirror near array)	491
<input type="checkbox"/>	L5	digital near optical near chemistry	15
	<i>DB=USPT; PLUR=NO; OP=OR</i>		
<input type="checkbox"/>	L4	5405783.pn.	1
<input type="checkbox"/>	L3	6066448.pn.	1
<input type="checkbox"/>	L2	6066448	19
<input type="checkbox"/>	L1	6586211.pn.	1

END OF SEARCH HISTORY

(FILE 'HOME' ENTERED AT 13:47:19 ON 14 JAN 2005)

FILE 'STNGUIDE' ENTERED AT 13:47:26 ON 14 JAN 2005

FILE 'HOME' ENTERED AT 13:47:31 ON 14 JAN 2005

FILE 'MEDLINE, CAPLUS, SCISEARCH, BIOSIS' ENTERED AT 13:47:42 ON 14 JAN 2005

L1 216 S MICROMIRROR ARRAY#
L2 19 S PHOTOLITHOGRAPH##### AND L1

FILE 'STNGUIDE' ENTERED AT 13:49:10 ON 14 JAN 2005

FILE 'MEDLINE, CAPLUS, SCISEARCH, BIOSIS' ENTERED AT 13:56:55 ON 14 JAN 2005

L3 12 DUPLICATE REMOVE L2 MEDLINE (7 DUPLICATES REMOVED)

FILE 'STNGUIDE' ENTERED AT 14:01:27 ON 14 JAN 2005

FILE 'MEDLINE, CAPLUS, SCISEARCH, BIOSIS' ENTERED AT 14:03:50 ON 14 JAN 2005

L4 E STAHLER CORD F/AU
6 S E2-E4

FILE 'STNGUIDE' ENTERED AT 14:05:47 ON 14 JAN 2005

FILE 'MEDLINE, CAPLUS, BIOSIS' ENTERED AT 14:07:31 ON 14 JAN 2005

FILE 'STNGUIDE' ENTERED AT 14:07:32 ON 14 JAN 2005

FILE 'MEDLINE, CAPLUS, SCISEARCH, BIOSIS' ENTERED AT 14:09:31 ON 14 JAN 2005

L5 E STAHLER PEER F/AU
15 S E1-E4
L6 11 DUPLICATE REMOVE L5 (4 DUPLICATES REMOVED)

FILE 'STNGUIDE' ENTERED AT 14:11:35 ON 14 JAN 2005

FILE 'MEDLINE, CAPLUS, SCISEARCH, BIOSIS' ENTERED AT 14:15:19 ON 14 JAN 2005

L7 E MULLER MANFRED/AU
0 S E3-EE7
L8 71 S E3-E7
L9 67 DUPLICATE REMOVE L8 (4 DUPLICATES REMOVED)
L10 0 S L9 AND MICROMIRROR
L11 5 S L9 AND ARRAY#

FILE 'STNGUIDE' ENTERED AT 14:17:47 ON 14 JAN 2005

FILE 'MEDLINE, CAPLUS' ENTERED AT 14:18:24 ON 14 JAN 2005

FILE 'STNGUIDE' ENTERED AT 14:18:24 ON 14 JAN 2005

FILE 'MEDLINE, CAPLUS' ENTERED AT 14:18:44 ON 14 JAN 2005

L12 E LINDNER HANS/AU
176 S E3-E12
L13 1 S L12 AND ARRAY#

FILE 'STNGUIDE' ENTERED AT 14:20:04 ON 14 JAN 2005

L4 ANSWER 1 OF 6 MEDLINE on STN
 AN 2003548843 MEDLINE
 DN PubMed ID: 14627841
 TI Validation of a novel, fully integrated and flexible microarray benchtop facility for gene expression profiling.
 AU Baum Michael; Biela Simone; Rittner Nicole; Schmid Kathrin; Eggelbusch Kathrin; Dahms Michael; Schlauersbach Andrea; Tahedl Harald; Beier Markus; Guimil Ramon; Scheffler Matthias; Hermann Carsten; Funk Jorg-Michael; Wixmerten Anke; Rebscher Hans; Honig Matthias; Andreae Claas; Buchner Daniel; Moschel Erich; Glathe Andreas; Jager Evelyn; Thom Marc; Greil Andreas; Bestvater Felix; Obermeier Frank; Burgmaier Josef; Thome Klaus; Weichert Sigrid; Hein Silke; Binnewies Tim; Foitzik Volker; Muller Manfred; **Stahler Cord Friedrich**; Stahler Peer Friedrich
 CS febit ag, Kafertaler Strasse 190, 68167 Mannheim, Germany.. michael.baum@febit.de
 SO Nucleic acids research, (2003 Dec 1) 31 (23) e151. Journal code: 0411011. ISSN: 1362-4962.
 CY England: United Kingdom
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 200406
 ED Entered STN: 20031121
 Last Updated on STN: 20040701
 Entered Medline: 20040630
 AB Here we describe a novel microarray platform that integrates all functions needed to perform any array-based experiment in a compact instrument on the researcher's laboratory benchtop. Oligonucleotide probes are synthesized in situ via a light-activated process within the channels of a three-dimensional microfluidic reaction carrier. Arrays can be designed and produced within hours according to the user's requirements. They are processed in a fully automatic workflow. We have characterized this new platform with regard to dynamic range, discrimination power, reproducibility and accuracy of biological results. The instrument detects sample RNAs present at a frequency of 1:100 000. Detection is quantitative over more than two orders of magnitude. Experiments on four identical arrays with 6398 features each revealed a mean coefficient of variation (CV) value of 0.09 for the 6398 unprocessed raw intensities indicating high reproducibility. In a more elaborate experiment targeting 1125 yeast genes from an unbiased selection, a mean CV of 0.11 on the fold change level was found. Analyzing the transcriptional response of yeast to osmotic shock, we found that biological data acquired on our platform are in good agreement with data from Affymetrix GeneChips, quantitative real-time PCR and--albeit somewhat less clearly--to data from spotted cDNA arrays obtained from the literature.
 CT Check Tags: Support, Non-U.S. Gov't
 Automation: IS, instrumentation
 *Gene Expression Profiling: IS, instrumentation
 Genes, Fungal: GE, genetics
 *Oligonucleotide Array Sequence Analysis: IS, instrumentation
 RNA, Fungal: AN, analysis
 RNA, Fungal: GE, genetics
 RNA, Messenger: AN, analysis
 RNA, Messenger: GE, genetics
 Reproducibility of Results
 Saccharomyces cerevisiae: GE, genetics
 Sensitivity and Specificity
 CN 0 (RNA, Fungal); 0 (RNA, Messenger)

L11 ANSWER 1 OF 5 MEDLINE on STN
 AN 2003548843 MEDLINE
 DN PubMed ID: 14627841
 TI Validation of a novel, fully integrated and flexible microarray benchtop facility for gene expression profiling.
 AU Baum Michael; Bielau Simone; Rittner Nicole; Schmid Kathrin; Eggelbusch Kathrin; Dahms Michael; Schlauersbach Andrea; Tahedl Harald; Beier Markus; Guimil Ramon; Scheffler Matthias; Hermann Carsten; Funk Jorg-Michael; Wixmerten Anke; Rebscher Hans; Honig Matthias; Andreae Claas; Buchner Daniel; Moschel Erich; Glathe Andreas; Jager Evelyn; Thom Marc; Greil Andreas; Bestvater Felix; Obermeier Frank; Burgmaier Josef; Thome Klaus; Weichert Sigrid; Hein Silke; Binnewies Tim; Foitzik Volker; **Muller Manfred**; Stahler Cord Friedrich; Stahler Peer Friedrich
 CS febit ag, Kafertaler Strasse 190, 68167 Mannheim, Germany..
 michael.baum@febit.de
 SO Nucleic acids research, (2003 Dec 1) 31 (23) e151.
 Journal code: 0411011. ISSN: 1362-4962.
 CY England: United Kingdom
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 200406
 ED Entered STN: 20031121
 Last Updated on STN: 20040701
 Entered Medline: 20040630
 AB Here we describe a novel microarray platform that integrates all functions needed to perform any **array**-based experiment in a compact instrument on the researcher's laboratory benchtop. Oligonucleotide probes are synthesized in situ via a light-activated process within the channels of a three-dimensional microfluidic reaction carrier. **Arrays** can be designed and produced within hours according to the user's requirements. They are processed in a fully automatic workflow. We have characterized this new platform with regard to dynamic range, discrimination power, reproducibility and accuracy of biological results. The instrument detects sample RNAs present at a frequency of 1:100 000. Detection is quantitative over more than two orders of magnitude. Experiments on four identical **arrays** with 6398 features each revealed a mean coefficient of variation (CV) value of 0.09 for the 6398 unprocessed raw intensities indicating high reproducibility. In a more elaborate experiment targeting 1125 yeast genes from an unbiased selection, a mean CV of 0.11 on the fold change level was found. Analyzing the transcriptional response of yeast to osmotic shock, we found that biological data acquired on our platform are in good agreement with data from Affymetrix GeneChips, quantitative real-time PCR and--albeit somewhat less clearly--to data from spotted cDNA **arrays** obtained from the literature.
 CT Check Tags: Support, Non-U.S. Gov't
 Automation: IS, instrumentation
 *Gene Expression Profiling: IS, instrumentation
 Genes, Fungal: GE, genetics
 *Oligonucleotide Array Sequence Analysis: IS, instrumentation
 RNA, Fungal: AN, analysis
 RNA, Fungal: GE, genetics
 RNA, Messenger: AN, analysis
 RNA, Messenger: GE, genetics
 Reproducibility of Results
 Saccharomyces cerevisiae: GE, genetics
 Sensitivity and Specificity
 CN 0 (RNA, Fungal); 0 (RNA, Messenger)

L13 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2005 ACS on STN
 AN 2000:253917 CAPLUS
 DN 133:144342
 ED Entered STN: 20 Apr 2000
 TI Trends and solutions in microarray production
 AU Kuhn, Claus; Dobler, Hannes; Klumpp, Bernhard; **Lindner, Hans**
 CS Fraunhofer Institut fur Produktionstechnik und Automatisierung, Stuttgart, Germany
 SO Bioforum International (2000), 4(1), 30-31
 CODEN: BINTFQ; ISSN: 1434-2693
 PB GIT Verlag GmbH
 DT Journal; General Review
 LA English
 CC 1-0 (Pharmacology)
 Section cross-reference(s): 3, 9, 20, 47, 63
 AB A review with 30 refs. In the pharmaceutical industry a large amount of money is spent for preclin. and clin. research. The development of one drug easily costs millions of dollars because hundreds and thousands of tests are being conducted. The demand for high-throughput and cost effective anal. of complex mixts. has led technol. toward the development and application of compact, high-d. **array** devices. So called biochips have numerous locations of different probes (=arrays), e. g. DNA-fragments, which allows for a multiparallel anal. of a sample. The information about the sequence of the DNA-fragment is related to the geometric location of the sample. Biochips are applied in gene expression, DNA-sequencing, immuno-diagnostics etc. The advantages of these biochips are: they require less reagent volume, they make anal. processes run faster because of their smaller size and they give the opportunity to implement more sensitive detection methods. By this they reduce costs, save time and improve quality. Different technologies are applied to create high d. **arrays** on the surface of a biochip. As printing technol. is very flexible, and promises a high step yield, the focus is on this technol. To create these high d. **arrays** certain requirements must be met concerning printing technol., handling technol., material and informational flow and environmental conditioning.
 ST review DNA microarray biochip prodn
 IT Biotechnology
 (biochips; trends and solns. in microarray production)
 IT DNA
 RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
 (microarrays; trends and solns. in microarray production)
 IT Drug screening
 Genetic mapping
 Pharmaceutical industry
 (trends and solns. in microarray production)
 RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD
 RE
 (1) Dobler, H; Trends and Solutions in Microarray Production 1999
 (2) Karri, L; Analytical Chemistry 1998, V70(7)
 (3) Marshall, A; Nature Biotechnology 1998, V16, P27 CAPLUS
 (4) Muller, M; TopSpot - A new Method for the Fabrication of BioChips 1999

L3 ANSWER 6 OF 12 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 2
 AN 2003:145559 CAPLUS
 DN 139:257447
 ED Entered STN: 26 Feb 2003
 TI Protein patterning by virtual mask **photolithography** using a
micromirror array
 AU Lee, Kook-Nyung; Shin, Dong-Sik; Lee, Yoon-Sik; Kim, Yong-Kweon
 CS School of Electrical Engineering and Computer Science, Seoul National
 University, S. Korea
 SO Journal of Micromechanics and Microengineering (2003), 13(1), 18-25
 CODEN: JMMIEZ; ISSN: 0960-1317
 PB Institute of Physics Publishing
 DT Journal
 LA English
 CC 9-1 (Biochemical Methods)
 AB The successful development of biosensors and protein chips requires a
 method for protein patterning on a solid surface. We describe a virtual
 mask photolithog. method for the surface patterning of proteins on a chip
 using a **micromirror array** (MMA) and its
 characterization. The excitation light was switched on or off using the
 MMA, and the light pattern was transferred using the pattern of
 switched-on mirrors. The nitroveratryloxycarbonyl (NVOC) group was
 utilized as a photolabile protecting group for protein patterning, so that
 biomols. could be immobilized on a patterned substrate. When illuminated
 by UV light, the photolabile protecting group was removed by a chemical
 reaction, and non-illuminated photolabile protecting groups protected the
 chip surface. Biotin was coupled only to the region where the protecting
 group had been removed, and so, biotin-streptavidin patterns were
 obtained. A two-dimensional MMA was designed and fabricated using
 micromachining technol. for use as a spatial light modulator. The
 projection system consisted of the MMA, a light source and other optical
 components, such as a projection lens. Fluorescein isothiocyanate was
 used to visualize the NVOC photo-cleavage sites and the
 biotin-streptavidin reaction. Parallel and quant. expts. required in the
 development of surface modification technol. for protein immobilization on
 a surface can easily be performed using this protein patterning system.
 ST protein immobilization patterning virtual mask photolithog
micromirror array
 IT Protein microarray technology
 (fabrication of; protein patterning by virtual mask photolithog. using
micromirror array)
 IT Proteins
 RL: ARU (Analytical role, unclassified); ANST (Analytical study)
 (immobilization of; protein patterning by virtual mask photolithog.
 using **micromirror array**)
 IT Mirrors
 (micro-; protein patterning by virtual mask photolithog. using
micromirror array)
 IT Immobilization, molecular or cellular
 (of protein; protein patterning by virtual mask photolithog. using
micromirror array)
 IT Plate glass
 RL: DEV (Device component use); USES (Uses)
 (protein immobilization on; protein patterning by virtual mask
 photolithog. using **micromirror array**)
 IT **Photolithography**
 (protein patterning by virtual mask photolithog. using
micromirror array)
 IT UV radiation
 (selective photo deprotection by; protein patterning by virtual mask
 photolithog. using **micromirror array**)

IT Surface
 (surface patterning; protein patterning by virtual mask photolithog. using **micromirror array**)

IT 27072-45-3D, Fluorescein isothiocyanate, conjugates with streptavidin
 RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
 (for visualization of array patterning; protein patterning by virtual mask photolithog. using **micromirror array**)

IT 58-85-5, Biotin 9013-20-1D, Streptavidin, conjugates with fluorescein isothiocyanate
 RL: ARU (Analytical role, unclassified); ANST (Analytical study)
 (protein patterning by virtual mask photolithog. using **micromirror array**)

IT 158641-92-0
 RL: DEV (Device component use); USES (Uses)
 (use as protecting reagent in protein immobilization; protein patterning by virtual mask photolithog. using **micromirror array**)

RE.CNT 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD
 RE

- (1) Ajayaghosh, A; Tetrahedron 1988, V44, P6661 CAPLUS
- (2) Bodanszky, M; Reactivity and Structure: Concepts in Organic Chemistry 1984, V21, P12
- (3) Buher, J; IEEE Microelectromech Syst 1997, V6, P126
- (4) Chung, S; Sensors Actuators A 1996, V54, P464
- (5) Jaecklin, V; Sensors Actuators A 1994, V43, P269 CAPLUS
- (6) Lee, K; J Micromech Microeng submitted
- (7) Lee, K; J Semicond Technol Sci 2001, V1, P132
- (8) Lee, K; SPIE 2001, P352 CAPLUS
- (9) Lispshutz, R; Biotechniques 1995, V19, P442
- (10) Pease, A; Proc Natl Acad Sci USA 1991, V91, P5022
- (11) Service, R; Science 1998, V282, P396 CAPLUS
- (12) Service, R; Science 1998, V282, P399 CAPLUS
- (13) Singh-Gasson, S; Nature Biotechnol 1999, V17, P974 CAPLUS
- (14) Storment, C; J Microelectromech Syst 1994, V3, P97
- (15) Wilchek, M; Methods in Enzymology 1990, V184, P5 CAPLUS